

GenCore version 5.1.4.P5.4578
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OM protein - protein search, using sw model

Run on: March 24, 2003, 16:07:11 ; Search time 36 Seconds

(without alignments)
1493.842 Million cell updates/sec

Title: US-09-988-971-2

Perfect score: 261
Sequence: 1 MGSLEPRRKLSPSPSSSSV.....RESLSFYISLDEAVSIDDA 261

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 671580 seqs, 206047115 residues

Word size: 0

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 100 summaries

Database:

SPTREMBL 21.*
1: sp. archaia.*
2: sp. bacteria.*
3: sp. fungi.*
4: sp. human.*
5: sp. invertebrate.*
6: sp. mammal.*
7: sp. mnc.*
8: sp. organelle.*
9: sp. phage.*
10: sp. plant.*
11: sp. rodent.*
12: sp. virus.*
13: sp. vertebrate.*
14: sp. unclassified.*
15: sp. virus.*
16: sp. bacteriophage.*
17: sp. archaea.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	261	100.0	261	4 Q9H6Q3	Q9H6Q3 homo sapien
2	197	75.5	197	4 Q9H135	Q9H135 homo sapien
3	178	68.2	210	4 Q9H118	Q9H118 homo sapien
4	63	24.1	63	4 Q96G14	Q96G14 homo sapien
5	37	14.2	179	11 Q9D129	Q9D129 mus musculu
6	37	14.2	259	11 Q8V142	Q8V142 mus musculu
7	37	14.2	259	11 Q8R4L0	Q8R4L0 mus musculu
8	9	3.4	423	4 Q8TDS5	Q8TDS5 mus musculu
9	9	3.4	505	4 Q8G1N1	Q8G1N1 mus musculu
10	8	3.1	64	4 Q8RC17	Q8RC17 mus sapien
11	8	3.1	93	6 Q9TUB7	Q9TUB7 mus sapien
12	8	3.1	135	4 Q9V779	Q9V779 mus sapien
13	8	3.1	138	12 Q8V8A2	Q8V8A2 mus sapien
14	8	3.1	161	4 Q9H817	Q9H817 mus sapien
15	8	3.1	177	4 P78453	P78453 mus sapien
16	8	3.1	178	16 Q98KH4	Q98KH4 rhizobium 1

17	17	8	3.1	217	11 Q9CX99	Q9CX99 mus musculu
18	18	8	3.1	217	13 Q9PU11	Q9PU11 xenopus lae
19	19	8	3.1	258	5 Q91709	Q91709 drosophila
20	20	8	3.1	276	4 Q13239	Q13239 homo sapien
21	21	8	3.1	280	11 Q8QZK8	Q8QZK8 mus musculu
22	22	8	3.1	281	11 Q60898	Q60898 mus musculu
23	23	8	3.1	447	5 Q94262	Q94262 caenorhabdi
24	24	8	3.1	461	11 Q63789	Q63789 rattus norv
25	25	8	3.1	467	5 Q77132	Q77132 hydra atten
26	26	8	3.1	488	13 Q13064	Q13064 xenopus lae
27	27	8	3.1	499	10 Q94AV6	Q94AV6 arabidopsis
28	28	8	3.1	502	13 Q9DDK6	Q9DDK6 salmo salar
29	29	8	3.1	506	11 Q62662	Q62662 rattus norv
30	30	8	3.1	512	11 Q61364	Q61364 mus musculu
31	31	8	3.1	512	11 Q61745	Q61745 mus musculu
32	32	8	3.1	512	11 Q922K9	Q922K9 mus musculu
33	33	8	3.1	517	11 Q63206	Q63206 rattus norv
34	34	8	3.1	697	3 Q8WZ33	Q8WZ33 neuropept
35	35	8	3.1	743	3 P87122	P87122 schizosacch
36	36	8	3.1	810	10 Q9FFK6	Q9FFK6 arabidopsis
37	37	8	3.1	827	5 Q9BL20	Q9BL20 caenorhabdi
38	38	7	2.7	17	4 Q9GZT7	Q9GZT7 homo sapien
39	39	7	2.7	40	4 Q9HCR6	Q9HCR6 homo sapien
40	40	7	2.7	61	4 Q9HCR7	Q9HCR7 homo sapien
41	41	7	2.7	70	10 Q9LW99	Q9LW99 pyrus pyrif
42	42	7	2.7	93	13 Q9PSU0	Q9PSU0 brachydanio
43	43	7	2.7	96	10 Q9C7L8	Q9C7L8 arabidopsis
44	44	7	2.7	102	4 Q8WUD9	Q8WUD9 homo sapien
45	45	7	2.7	106	16 Q55970	Q55970 synecocyst
46	46	7	2.7	109	11 Q9DAJ0	Q9DAJ0 mus musculu
47	47	7	2.7	114	16 Q9S572	Q9S572 pseudomonas
48	48	7	2.7	115	16 Q8V8M4	Q8V8M4 listeria mo
49	49	7	2.7	117	4 Q9HUF7	Q9HUF7 homo sapien
50	50	7	2.7	118	16 Q92FH6	Q92FH6 listeria in
51	51	7	2.7	127	5 Q9NLP4	Q9NLP4 leishmania
52	52	7	2.7	128	11 Q9D980	Q9D980 mus musculu
53	53	7	2.7	136	16 Q9PFA8	Q9PFA8 xyella fas
54	54	7	2.7	140	16 Q8UH38	Q8UH38 agrobacteri
55	55	7	2.7	154	12 Q69596	Q69596 hepatitis b
56	56	7	2.7	172	10 Q94H66	Q94H66 oryza sativ
57	57	7	2.7	177	4 Q8WMB3	Q8WMB3 homo sapien
58	58	7	2.7	179	10 Q9AS32	Q9AS32 oryza sativ
59	59	7	2.7	180	16 Q915V4	Q915V4 pseudomonas
60	60	7	2.7	181	4 Q9HCR8	Q9HCR8 homo sapien
61	61	7	2.7	188	16 Q92V87	Q92V87 rhizobium m
62	62	7	2.7	189	10 Q9C5Z4	Q9C5Z4 arabidopsis
63	63	7	2.7	189	10 Q9SCS9	Q9SCS9 arabidopsis
64	64	7	2.7	189	10 Q8K144	Q8K144 solanum tub
65	65	7	2.7	192	17 Q8ZV47	Q8ZV47 pyrobaculum
66	66	7	2.7	193	17 Q9V206	Q9V206 pyrococcus
67	67	7	2.7	198	5 Q9U4D4	Q9U4D4 caenorhabdi
68	68	7	2.7	200	11 Q9D387	Q9D387 mus musculu
69	69	7	2.7	201	16 Q84606	Q84606 chlamydia t
70	70	7	2.7	201	2 Q87962	Q87962 streptomyce
71	71	7	2.7	202	16 Q9PUD9	Q9PUD9 chlamydia m
72	72	7	2.7	206	4 Q9P0N6	Q9P0N6 homo sapien
73	73	7	2.7	217	16 Q8X862	Q8X862 escherichia
74	74	7	2.7	219	10 Q9Y0F6	Q9Y0F6 thalassios
75	75	7	2.7	219	16 Q9CJ13	Q9CJ13 lactococcus
76	76	7	2.7	224	11 Q9DC70	Q9DC70 mus musculu
77	77	7	2.7	227	8 Q9WEC3	Q9WEC3 pythium ult
78	78	7	2.7	234	10 Q8W320	Q8W320 oryza sativ
79	79	7	2.7	237	10 Q9LKG0	Q9LKG0 lycopersico
80	80	7	2.7	245	16 Q9RV09	Q9RV09 delnococeus
81	81	7	2.7	248	16 Q8URF9	Q8URF9 agrobacteri
82	82	7	2.7	251	10 Q8S241	Q8S241 oryza sativ
83	83	7	2.7	257	10 Q9LRL6	Q9LRL6 arabidopsis
84	84	7	2.7	257	11 Q9DAP6	Q9DAP6 mus musculu
85	85	7	2.7	262	17 Q8TKL4	Q8TKL4 methanosaic
86	86	7	2.7	267	10 Q9SXK8	Q9SXK8 arabidopsis
87	87	7	2.7	269	16 Q92W32	Q92W32 rhizobium m
88	88	7	2.7	270	10 Q94ZP5	Q94ZP5 oryza sativ
89	89	7	2.7	273	10 Q9S0U4	Q9S0U4 brisealica ca

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90 7 2.7 275 16 099UZ5 099UZ5 staphylococ
91 7 2.7 276 2 08RX90 08RX90 micrococci
92 7 2.7 278 2 053603 053603 streptomyce
93 7 2.7 278 16 050890 050890 borrelia bu
94 7 2.7 278 16 09RXU5 09RXU5 deinococcus
95 7 2.7 278 16 050889 050889 borrelia bu
96 7 2.7 284 3 060156 060156 schizosacch
97 7 2.7 287 16 09PKP4 09PKP4 chlamydia m
98 7 2.7 293 4 09BQ87 09BQ87 homo sapien
99 7 2.7 294 16 09KX01 09KX01 vibrio chol
100 7 2.7 294 16 09PNF4 09PNF4 campylobact

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ALIGNMENTS

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RESULT 1
09H603 PRELIMINARY; PRT; 261 AA.

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AC 09H603;
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 21, Last annotation update)
DE CDNA: FJ21992 f16, clone HEP06554 (Src-like adapter protein-2)
DE (Modulator of antigen receptor signaling MARS).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kawabata A., Hiki T., Kobatake N., Itagaki H., Ikema Y., Okamoto S.,
RA Okitani R., Oca T., Suzuki Y., Odayashi M., Nishi T., Shibahara T.,
RA Tanaka T., Nakamura Y., Isogai T., Sugano S.,
RT "NEDO human cDNA sequencing project."
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.

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RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE=21553259; PubMed=1196592;
RA Holland S.J., Liao X.C., Mendenhall M.K., Zhou X., Pardo J., Chu P.,
RA Spencer C., Fu A.C., Sheng N., Yu P., Pail E., Nagin A., Shen M.,
RA Yu S., Chan E., Wu X., Li C., Wolsetschlager M., Aversa G.,
RA Kolbinger F., Bennett M.K., Molinaux S., Luo Y., Payan D.G.,
RA Manabe H.S.Y., Wu J.,
RT "Functional cloning of Src-like Adapter Protein-2 (SLAP-2), a Novel
RT Inhibitor of Antigen Receptor Signaling."
RL J. Exp. Med. 194:1263-1276(2001).

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RN [3]
RP SEQUENCE FROM N.A.
RA TISSUE=THYMUS;
RA Loreto M.P., McGlade C.J.,
RT "Modulator of Antigen Receptor Signaling (MARS).";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
DR EMBL: AK025645; BA015201.1; -
DR EMBL: AF326353; AAL29204.1; -
DR EMBL: AF290985; AAL38197.1; -
DR HSSP: P06239; ILKK.
DR InterPro: IPR000980; SH2.
DR InterPro: IPR001452; SH3.
DR Pfam: PF00017; SH2; 1.
DR Pfam: PF00018; SH3; 1.
DR PRINTS: PR00401; SH2DOMAIN.
DR ProDom: PD000093; SH2; 1.
DR SMART: SM00252; SH2; 1.
DR SMART: SM00326; SH3; 1.
DR PROSITE: PS00001; SH2; 1.
DR PROSITE: PS00002; SH3; 1.
KW SH3 domain; Receptor.
SQ SEQUENCE 261 AA; 28585 MW; 858AF03451672B3D CRC64;

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Query Match 100.0%; Score 261; DB 4; Length 261;
Best Local Similarity 100.0%; Pred. No. 1,7e-254;

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Matches 261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MGSLPSRRKSLPSPSSSSVGGPGVPTMEAESKATPAVALGSPAGAPALSLRIGEPIT 60
1 MGSLPSRRKSLPSPSSSSVGGPGVPTMEAESKATPAVALGSPAGAPALSLRIGEPIT 60
Db 1 MGSLPSRRKSLPSPSSSSVGGPGVPTMEAESKATPAVALGSPAGAPALSLRIGEPIT 60
Qy 61 IVSDGDMTVLSEVSGREYNIPIVHAKVSHGMVYEGLSREKAEELLPLPGPGAFLL 120
61 IVSDGDMTVLSEVSGREYNIPIVHAKVSHGMVYEGLSREKAEELLPLPGPGAFLL 120
Db 61 IVSDGDMTVLSEVSGREYNIPIVHAKVSHGMVYEGLSREKAEELLPLPGPGAFLL 120
Qy 121 RESQTRRGYSLSVRLSPASMDRIHRYRIHCLDNGWLYISPLTPPSIQALVDHYSLEA 180
121 RESQTRRGYSLSVRLSPASMDRIHRYRIHCLDNGWLYISPLTPPSIQALVDHYSLEA 180
Db 121 RESQTRRGYSLSVRLSPASMDRIHRYRIHCLDNGWLYISPLTPPSIQALVDHYSLEA 180
Qy 181 DIICCLKEPCVQORAGPLPGKDIPLVTVQRTPLNWKELDSILFSEAAATGEESLSEG 240
181 DIICCLKEPCVQORAGPLPGKDIPLVTVQRTPLNWKELDSILFSEAAATGEESLSEG 240
Db 181 DIICCLKEPCVQORAGPLPGKDIPLVTVQRTPLNWKELDSILFSEAAATGEESLSEG 240
Qy 241 LRESISFYISLNDVAVSLLDDA 261
241 LRESISFYISLNDVAVSLLDDA 261
Db 241 LRESISFYISLNDVAVSLLDDA 261

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RESULT 2
09H135 PRELIMINARY; PRT; 197 AA.

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AC 09H135;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 20, Last annotation update)
DE D1977B1.1 (Novel protein tyrosine kinase with Src homology domain 2
DE (SH2) domains) (Fragment).
GN D1977B1.1
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Lloyd D.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AL050318; CAB75365.1; -
DR HSSP: P06239; ILKK.
DR InterPro: IPR000980; SH2.
DR Pfam: PF00017; SH2; 1.
DR PRINTS: PR00401; SH2DOMAIN.
DR ProDom: PD000093; SH2; 1.
DR SMART: SM00252; SH2; 1.
DR PROSITE: PS00001; SH2; 1.
DR KINASE.
KW NON_TER
FT
SQ SEQUENCE 197 AA; 22124 MW; EF01FE7A85C5C1F1 CRC64;

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Query Match 75.5%; Score 197; DB 4; Length 197;
Best Local Similarity 100.0%; Pred. No. 4.2e-190;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 65 DDDMMTVLSEVSGREYNIPIVHAKVSHGMVYEGLSREKAEELLPLPGPGAFLLRISQ 124
65 DDDMMTVLSEVSGREYNIPIVHAKVSHGMVYEGLSREKAEELLPLPGPGAFLLRISQ 124
Db 1 DDDMMTVLSEVSGREYNIPIVHAKVSHGMVYEGLSREKAEELLPLPGPGAFLLRISQ 60
Qy 125 TRRGYSLSVRLSPASMDRIHRYRIHCLDNGWLYISPLTPPSIQALVDHYSLEADIC 184
125 TRRGYSLSVRLSPASMDRIHRYRIHCLDNGWLYISPLTPPSIQALVDHYSLEADIC 184
Db 61 TRRGYSLSVRLSPASMDRIHRYRIHCLDNGWLYISPLTPPSIQALVDHYSLEADIC 120
Qy 185 CLIKPCVQLQAGPLPGKDIPLVTVQRTPLNWKELDSILFSEAAATGEESLSEGRES 244
185 CLIKPCVQLQAGPLPGKDIPLVTVQRTPLNWKELDSILFSEAAATGEESLSEGRES 244
Db 121 CLIKPCVQLQAGPLPGKDIPLVTVQRTPLNWKELDSILFSEAAATGEESLSEGRES 180
Qy 245 LSFYISLNDVAVSLLDDA 261
245 LSFYISLNDVAVSLLDDA 261
Db 181 LSFYISLNDVAVSLLDDA 197

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RESULT 3
ID 08WY18 PRELIMINARY; PRT; 210 AA.
AC 08WY18;
DT 01-MAR-2002 (TEMBLrel. 20, Created)
DT 01-MAR-2002 (TEMBLrel. 20, Last sequence update)
DE 01-JUN-2002 (TEMBLrel. 21, Last annotation update)
DE Modulator of antigen receptor signaling, putative splice isoform
DE MARS-v.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=THYMUS;
RT Loreto M.P., McGlade C.J.;
RT "Modulator of Antigen Receptor Signaling (MARS) - putative splice
RT variant."
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF290986; AAL36198.1;
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001452; SH1.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF00018; SH3; 1.
DR PRINTS; PRO0401; SH2DOMAIN.
DR PRINTS; PRO0452; SH3DOMAIN.
DR ProDom; PD000093; SH2; 1.
DR SMART; SM00252; SH2; 1.
DR SMART; SM00326; SH3; 1.
DR PROSITE; PSS0001; SH2; 1.
DR PROSITE; PSS0002; SH3; 1.
KW Receptor.
SQ SEQUENCE 210 AA; 23103 MW; BED62208E53A472E CRC64;

Query Match 68.2%; Score 178; DB 4; Length 210;
Best Local Similarity 100.0%; Pred. No. 6,2e-171;
Matches 178; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGSLPSRRKSLSPSSLSVSSVGGQGPVTMEAEERSKATVAVALGSPAGPAELSLRGEPLT 60
DB 1 MGSLPSRRKSLSPSSLSVSSVGGQGPVTMEAEERSKATVAVALGSPAGPAELSLRGEPLT 60

QY 61 IVSEBDGMWTVLSEVSGREYIPSYHVAKVSHGMYEGLSREKAEELLILPGNPGCAFPI 120
DB 61 IVSEBDGMWTVLSEVSGREYIPSYHVAKVSHGMYEGLSREKAEELLILPGNPGCAFPI 120

QY 121 RESQTRRGSYSLSVRLSPAPSWDRIRHRIHCHDNGMLYISRLTPPSLQALVDHYSE 178
DB 121 RESQTRRGSYSLSVRLSPAPSWDRIRHRIHCHDNGMLYISRLTPPSLQALVDHYSE 178

RESULT 4
ID 096Q14 PRELIMINARY; PRT; 63 AA.
AC 096Q14;
DT 01-DEC-2001 (TEMBLrel. 19, Created)
DT 01-DEC-2001 (TEMBLrel. 19, Last sequence update)
DE 01-DEC-2001 (TEMBLrel. 19, Last annotation update)
DE DJ460J8.2 (Novel protein tyrosine kinase with Src homology 2 (SH2)
DE domain) (Fragment).
GN DJ977B1.1.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Skuce C.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
KW EMBL; AL031662; CAC44645.1; -.
kinase.

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FT NON TER 63 63
SQ SEQUENCE 63 AA; 6350 MW; 3EC599C9F1723053 CRC64;

Query Match 24.1%; Score 63; DB 4; Length 63;
Best Local Similarity 100.0%; Pred. No. 1.7e-55;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGSLPSRRKSLSPSSLSVSSVGGQGPVTMEAEERSKATVAVALGSPAGPAELSLRGEPLT 60
DB 1 MGSLPSRRKSLSPSSLSVSSVGGQGPVTMEAEERSKATVAVALGSPAGPAELSLRGEPLT 60

QY 61 IVS 63
DB 61 IVS 63

RESULT 5
ID 09D129 PRELIMINARY; PRT; 179 AA.
AC 09D129;
DT 01-JUN-2001 (TEMBLrel. 17, Created)
DT 01-JUN-2001 (TEMBLrel. 17, Last sequence update)
DE 01-JUN-2002 (TEMBLrel. 21, Last annotation update)
DE A930009E21R1K protein.
GN A930009E21R1K.
OS Mus musculus (mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=RETINA;
RX MEDLINE=21085660; PubMed=11217651;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arikawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batelov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirral L.M., Stanbaj F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carinci P., de Bonaio M.F.,
RA Brownstein M.D., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Guetincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyoko-Oka K., Wang K.H., Weitz C., Whitlaker C., Wilming L.,
RA Wyszewski B., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
RA Hayashizaki Y.,
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
DR EMBL; AK020837; BAB32223.1; -.
DR HSSP; P06239; ILKK.
DR MGD; MGI:1925049; A930009E21R1K.
DR InterPro; IPR000980; SH2.
DR Pfam; PF00017; SH2; 1.
DR PRINTS; PRO0401; SH2DOMAIN.
DR ProDom; PD000093; SH2; 1.
DR SMART; SM00252; SH2; 1.
DR PROSITE; PSS0001; SH2; 1.
SQ SEQUENCE 179 AA; 19926 MW; 60477A0CF4003FDC CRC64;

Query Match 14.2%; Score 37; DB 11; Length 179;
Best Local Similarity 100.0%; Pred. No. 6.9e-29;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 92 HGWLYEGLSREKAEELLILPGNPGCAFPIRESQTRRG 128
DB 11 HGWLYEGLSREKAEELLILPGNPGCAFPIRESQTRRG 47

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RESULT 6

Q8V142 PRELIMINARY; PRT; 259 AA.

ID 08V142
AC 08V142
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Modulator of antigen receptor signaling MARS.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Loreto M.P., McGlade C.J.,
RT "Modulator of Antigen Receptor Signaling (MARS).",
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF287467; AAL38196.1; -
DR InterPro: IPR000980; SH2.
DR InterPro: IPR001452; SH3.
DR Pfam: PF00017; SH2; 1.
DR Pfam: PF00018; SH3; 1.
DR PRINTS; PR00401; SH2DOMAIN.
DR PRINTS; PR00452; SH2DOMAIN.
DR ProDom: PD000093; SH2; 1.
DR SMART; SM00252; SH2; 1.
DR SMART; SM00326; SH3; 1.
DR PROSITE; PS50001; SH2; 1.
DR PROSITE; PS50002; SH3; 1.
KM RECEPTOR.
SQ SEQUENCE 259 AA; 28476 MW; 8270F17CD3FC50A3 CRC64;

Query Match 14.2%; Score 37; DB 11; Length 259;
Best Local Similarity 100.0%; Pred. No. 9, 7e-29;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 92 HGMVLEGLSRKAEELLIPGNPGAFILRESQTRG 128
DB 91 HGMVLEGLSRKAEELLIPGNPGAFILRESQTRG 127

RESULT 7

ID 08R410 PRELIMINARY; PRT; 259 AA.

AC 08R410
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Src-like adapter protein-2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Pandey A., Ibarrola N., Kratchmarova I., Fernandez M.,
RA Constantinescu S., Ohara O., Sawaedkiosol S., Lodish H.F., Mann M.,
RT "A novel Src homology 2 domain-containing molecule, Src-Like Adapter
RT Protein-2 (SLAP-2), which negatively regulates T cell receptor
RT signaling".
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Ibarrola N., Mann M., Pandey A.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF434990; AAL86403.1; -
SQ SEQUENCE 259 AA; 28516 MW; 1388E8244152B34 CRC64;

Query Match 14.2%; Score 37; DB 11; Length 259;
Best Local Similarity 100.0%; Pred. No. 9, 7e-29;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 92 HGMVLEGLSRKAEELLIPGNPGAFILRESQTRG 128

DB 91 HGMVLEGLSRKAEELLIPGNPGAFILRESQTRG 127

RESULT 8

ID 08TDS5 PRELIMINARY; PRT; 423 AA.

AC 08TDS5
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Putative G-protein coupled receptor.
CN GPCR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
CX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Takeda S., Kadowaki S., Haga T., Takaesu H., Mitaku S.;
RT "Identification of G protein-coupled receptor genes from the human
RL genome sequence.",
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB083630; BAB89343.1; -
KM RECEPTOR.
SQ SEQUENCE 423 AA; 45810 MW; 72ADA9F43A9EC051 CRC64;

Query Match 3.4%; Score 9; DB 4; Length 423;
Best Local Similarity 100.0%; Pred. No. 2, 5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 PSPSLSSSV 20
DB 48 PSPSLSSSV 56

RESULT 9

ID 0961N1 PRELIMINARY; PRT; 505 AA.

AC 0961N1
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Unknown (protein for MGC:16168).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
CX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RA Strausberg R.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC007371; AAH07371.1; -
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR000980; SH2.
DR InterPro: IPR001452; SH3.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00018; SH2; 1.
DR Pfam; PF00018; SH3; 1.
DR ProDom: PD000001; Euk_pkinase; 1.
DR ProDom: PD000066; SH3; 1.
DR ProDom: PD000093; SH2; 1.
DR ProDom: PD000107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS50001; SH2; 1.
DR PROSITE; PS50002; SH3; 1.
KM ATP-binding; Transferase.
SQ SEQUENCE 505 AA; 57706 MW; B5F739BEF8389176 CRC64;

Query Match 3.4%; Score 9; DB 4; Length 505;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 165 TPEPQLALV 173
 |||||
 DB 194 TPEPQLALV 202

RESULT 10

08TC17 PRELIMINARY; PRT; 64 AA.
 AC 08TC17
 DT 01-JUN-2002 (TREMBlrel. 21, Created)
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Hypothetical 7.2 kDa protein (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LUNG;
 RA Strauberg R.;
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC026233; AAH26233.1; -
 KW Hypothetical protein.
 FT NON TER 1
 SQ SEQUENCE 64 AA; 7183 MW; 0D8C6FF43E221DC CRC64;

Query Match 3.1%; Score 8; DB 4; Length 64;
 Best Local Similarity 100.0%; Pred. No. 4.5;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 116 GAFLIRS 123
 |||||
 DB 29 GAFLIRS 36

RESULT 11

09TUB7 PRELIMINARY; PRT; 93 AA.
 AC 09TUB7
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE Growth factor receptor-bound protein 2 (Fragment).
 OS Ursus maritimus (Polar bear) (Tralacros maritimus).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Ursus.
 NCBI_TaxID=29073;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Libertes D.A., Schreiber D.R., Chamberlin S.G., Govindarajan S.,
 RA Thomson J.M., Wigger M., Benner S.A.;
 RT "Evolutionary Analysis of the Src Homology 2 (SH2) Domain."
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF093133; AAF03915.1; -
 DR HSSP: P29354; 1BMB.
 DR InterPro: IPR000980; SH2.
 DR Pfam: PF00017; SH2; 1.
 DR PRINTS: PR00401; SH2DOMAIN.
 DR PRODOM: PD000093; SH2; 1.
 DR SMART: SMO0252; SH2; 1.
 DR PROSITE: PSS0001; SH2; 1.
 KW Receptor.
 FT NON TER 1
 FT NON TER 93
 SQ SEQUENCE 93 AA; 10837 MW; 3546DCC1E1A1FE3A CRC64;

Query Match 3.1%; Score 8; DB 6; Length 93;
 Best Local Similarity 100.0%; Pred. No. 6.4;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 116 GAFLIRS 123

DB 22 GAFLIRS 29
 |||||

RESULT 12

099779 PRELIMINARY; PRT; 135 AA.
 AC 099779
 DT 01-MAY-1997 (TREMBlrel. 03, Created)
 DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Hypothetical 14.4 kDa protein (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BRAIN;
 RA MEDLINE=96207227; PubMed=8619474;
 RA Anderson B., Wentland M.A., Ricafrente J.Y., Liu W., Gibbs R.A.;
 RT "A 'double adaptor' method for improved shotgun library
 RT construction.";
 RL Anal. Biochem. 236:107-113 (1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BRAIN;
 RA MEDLINE=97264341; PubMed=9110174;
 RA Yu W., Andersson B., Worley K.C., Muzny D.M., Ding Y., Liu W.,
 RA Ricafrente J.Y., Wentland M.A., Lennon G., Gibbs R.A.;
 RT "Large-scale concatenation cDNA sequencing.";
 RL Genome Res. 7:353-358 (1997).
 DR EMBL: U79280; AAB50218.1; -
 KW Hypothetical protein.
 FT NON TER 1
 SQ SEQUENCE 135 AA; 14406 MW; D4B7C08054BF41C7 CRC64;

Query Match 3.1%; Score 8; DB 4; Length 135;
 Best Local Similarity 100.0%; Pred. No. 9;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 37 AVAGSFP 44
 |||||
 DB 101 AVAGSFP 108

RESULT 13

08VAS2 PRELIMINARY; PRT; 138 AA.
 AC 08VAS2
 DT 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Wsv320 (WSSV376).
 OS White spot syndrome virus (WSSV).
 OC Viruses; unclassified viruses.
 NCBI_TaxID=92652;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=21548311; PubMed=11689662;
 RA Yang F., He J., Lin X., Li Q., Pan D., Zhang X., Xu X.;
 RT "Complete genome sequence of the shrimp white spot bacilliform
 RT virus.";
 RL J. Virol. 75:11811-11820 (2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Yang F., He J., Lin X., Li Q., Pan D., Zhang X., Xu X.;
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TAIWAN;
 RX MEDLINE=20517548; PubMed=11062040;
 RX Tsai M.F., Yu H.T., Tzeng H.F., Lwu J.H., Chou C.M., Huang C.J.,

RA Wang C.H., Lin J.Y., Kou G.H., Lo C.F.;
 RT "Identification and characterization of a shrimp white spot syndrome
 RT virus (WSSV) gene that encodes a novel chimeric polypeptide of
 RT cellular-type thymidine kinase and thymidylate kinase."
 RL Virology 277:100-110(2000).

RN [4]
 RP SEQUENCE FROM N.A.

RC STRAIN=TAIWAN;

RX MEDLINE=21844071; PubMed=11853398;

RA Chen L.T., Liu J.H., Huang C.J., Chou C.M., Chen S.M., Wang C.H.,

Lo C.F., Kou G.H.;

RT "Identification of a nucleocapsid protein (VP35) gene of shrimp white
 RT spot syndrome virus and characterization of the motif important for
 RT targeting VP35 to the nuclei of transfected insect cells."
 RL Virology 293:44-53(2002).

RN [5]
 RP SEQUENCE FROM N.A.

RC STRAIN=TAIWAN;

RA Lo C.-F., Kou G.-H.;

RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF332093; AAI3322.1; -

DR EMBL: AF440570; AAL89244.1; -

SO SEQUENCE 138 AA; 13970 MW; 8A3ABC08BD8E804B CRC64;

QY 12 PPSLSSS 19

DB 58 PPSLSSS 65

QY 12 PPSLSSS 19

DB 58 PPSLSSS 65

QY 12 PPSLSSS 19

DB 58 PPSLSSS 65

QY 12 PPSLSSS 19

DB 58 PPSLSSS 65

QY 12 PPSLSSS 19

DB 58 PPSLSSS 65

QY 12 PPSLSSS 19

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QY 12 PPSLSSS 19

DB 58 PPSLSSS 65

QY 12 PPSLSSS 19

DB 58 PPSLSSS 65

QY 12 PPSLSSS 19

DB 58 PPSLSSS 65

QY 12 PPSLSSS 19

DB 58 PPSLSSS 65

QY 12 PPSLSSS 19

DB 58 PPSLSSS 65

QY 12 PPSLSSS 19

Query Match 3.1%; Score 8; DB 4; Length 161;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 159 YISPRITF 166

DB 143 YISPRITF 150

QY 159 YISPRITF 166

DB 143 YISPRITF 150

QY 159 YISPRITF 166

DB 143 YISPRITF 150

QY 159 YISPRITF 166

DB 143 YISPRITF 150

QY 159 YISPRITF 166

DB 143 YISPRITF 150

QY 159 YISPRITF 166

DB 143 YISPRITF 150

QY 159 YISPRITF 166

DB 143 YISPRITF 150

QY 159 YISPRITF 166

DB 143 YISPRITF 150

QY 159 YISPRITF 166

DB 143 YISPRITF 150

QY 159 YISPRITF 166

DB 143 YISPRITF 150

QY 159 YISPRITF 166

DB 143 YISPRITF 150

QY 159 YISPRITF 166

DB 143 YISPRITF 150

QY 159 YISPRITF 166

DB 143 YISPRITF 150

QY 159 YISPRITF 166

DB 143 YISPRITF 150

QY 159 YISPRITF 166

DB 143 YISPRITF 150

QY 159 YISPRITF 166

DB 143 YISPRITF 150

QY 159 YISPRITF 166

DB 143 YISPRITF 150

QY 159 YISPRITF 166

DB 143 YISPRITF 150

QY 159 YISPRITF 166

DB 143 YISPRITF 150

QY 159 YISPRITF 166

DB 143 YISPRITF 150

QY 159 YISPRITF 166

DB 143 YISPRITF 150

QY 159 YISPRITF 166

DB 143 YISPRITF 150

QY 159 YISPRITF 166

DB 143 YISPRITF 150

QY 159 YISPRITF 166

DB 143 YISPRITF 150

QY 159 YISPRITF 166

DB 143 YISPRITF 150

QY 159 YISPRITF 166

DB 143 YISPRITF 150

QY 159 YISPRITF 166

DB 143 YISPRITF 150

QY 159 YISPRITF 166

DB 143 YISPRITF 150

QY 159 YISPRITF 166

DB 143 YISPRITF 150

QY 159 YISPRITF 166

DB 143 YISPRITF 150

QY 159 YISPRITF 166

DB 143 YISPRITF 150

QY 159 YISPRITF 166

DB 143 YISPRITF 150

QY 159 YISPRITF 166

DB 143 YISPRITF 150

QY 159 YISPRITF 166

DB 143 YISPRITF 150

QY 159 YISPRITF 166

DB 143 YISPRITF 150

QY 159 YISPRITF 166

DB 143 YISPRITF 150

QY 159 YISPRITF 166

DB 143 YISPRITF 150

QY 159 YISPRITF 166

DB 143 YISPRITF 150

QY 159 YISPRITF 166

DB 143 YISPRITF 150

QY 159 YISPRITF 166

DB 143 YISPRITF 150

GN MRL1474.
 OS Rhizobium loci (Mesorhizobium loci).
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Phyllobacteriaceae; Mesorhizobium.
 OX NCBI_TaxID=381;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MAFP303099;
 RX MEDLINE=21082930; PubMed=11214968;
 RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Saemoto S.,
 RA Matenabe A., Idegawa K., Ishikawa A., Kawashima K., Kimura T.,
 RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
 RA Koshizuki Y., Nakayama S., Nakazaki N., Shimpō S., Sugimoto M.,
 RA Takeuchi C., Yamada M., Tabata S.;
 RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
 RT Mesorhizobium loci."
 RT DNA Res. 7:331-338 (2000).
 DR EMBL, AF002997; BAB48840.1;
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 178 AA; 19823 MW; EB4B7DEB9D36ED46 CRC64;
 Query Match 3.1%; Score 8; DB 16; Length 178;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 57 EPTTVSE 64
 DB 133 EPTTVSE 140
 RESULT 17
 O9CX99 PRELIMINARY; PRT; 217 AA.
 AC O9CX99.
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE 8430435N19Rik protein.
 GN GRAP OR 8430435N19Rik.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=EMBRYONIC LUNG;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
 RA Aizawa K., Iwata M., Nishi K., Kiyosawa H., Kondo S., Yamana K.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kanukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batilov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bulc C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kaniya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mondaeris P.,
 RA Norone P., Ring B., Ringwald W., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection."
 RT Nature 409:685-690(2001).
 RL Nature 409:685-690(2001).
 CC -1- SIMILARITY: CONTAINS 2 SH3 DOMAINS.
 DR EMBL, AK018457; BAB31222.1; -.
 DR HSSP, P29354; 1BM2.
 DR MGD; MGI:191870; Grap.
 DR InterPro; IPR000108; Neu_cyt_fac2_2.
 DR InterPro; IPR000980; SH2.

DR InterPro; IPR001452; SH3.
 DR Pfam; PF00017; SH2; 1.
 DR Pfam; PF00018; SH3; 2.
 DR PRINTS; PR00499; P67PHOX.
 DR PRINTS; PR00401; SH2DOMAIN.
 DR PRINTS; PR00452; SH3DOMAIN.
 DR PRODOM; PD000066; SH3; 2.
 DR PRODOM; PD000093; SH2; 1.
 DR SMART; SM00252; SH2; 1.
 DR SMART; SM00326; SH3; 2.
 DR PROSITE; PS50001; SH2; 1.
 DR PROSITE; PS50002; SH3; 2.
 DR SH3 domain.
 SQ SEQUENCE 217 AA; 25277 MW; 1AF124C3D2773DD2 CRC64;
 Query Match 3.1%; Score 8; DB 11; Length 217;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 116 GAFLIRS 123
 DB 81 GAFLIRS 88
 RESULT 18
 O9PUL1 PRELIMINARY; PRT; 217 AA.
 AC O9PUL1.
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Grb2 protein.
 GN GRB2.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodidae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Gollaset C., Shi D.L., Boucancut J.C.;
 RT "Selective inhibition of neural induction but not mesoderm induction
 RT by interfering mutants of Sem-5/Grb2."
 RL Submitted (DEC-1997) to the EMBL/Genbank/DBJ databases.
 CC -1- SIMILARITY: CONTAINS 2 SH3 DOMAINS.
 DR EMBL; AJ23061; CAB59279.1; -.
 DR HSSP; P29354; 1GHU.
 DR InterPro; IPR000108; Neu_cyt_fac2_2.
 DR InterPro; IPR000980; SH2.
 DR InterPro; IPR001452; SH3.
 DR Pfam; PF00017; SH2; 1.
 DR Pfam; PF00018; SH3; 2.
 DR PRINTS; PR00499; P67PHOX.
 DR PRINTS; PR00401; SH2DOMAIN.
 DR PRINTS; PR00452; SH3DOMAIN.
 DR PRODOM; PD000066; SH3; 2.
 DR PRODOM; PD000093; SH2; 1.
 DR SMART; SM00252; SH2; 1.
 DR SMART; SM00326; SH3; 2.
 DR PROSITE; PS50001; SH2; 1.
 DR PROSITE; PS50002; SH3; 2.
 DR SH3 domain.
 SQ SEQUENCE 217 AA; 25135 MW; 2349A68260F9D4CD CRC64;
 Query Match 3.1%; Score 8; DB 13; Length 217;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 116 GAFLIRS 123
 DB 81 GAFLIRS 88

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RESULT 19
Q91709          PRELIMINARY;      PRT;      258 AA.
AC Q91709;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE CG16778 protein.
GN CG16778.
OS Drosophila melanogaster (fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephyridae; Drosophilidae; Drosophila.
OK NCBI_TaxId=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Aghayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,
RA Borkov D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K.J., Doug L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fostler A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,
RA Jajai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mallet B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pauley J.M.,
RA Palenzuela M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kimios I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svitek R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock K.C., Wu D., Yang S., Yao Q.A.,
RA Williams S.M., Woodage T., Worley K.C., Xu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zhang L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
DR EMBL; AE003466; AAG2201.1; -
DR FLYBase; FBgn0035093; CG16778.
SQ SEQUENCE 258 AA; 28886 MW; 4BD0181BF414FB2 CRC64;

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Query Match          3.1%; Score 8; DB 5; Length 258;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 13 SPSSSSV 20
DB 219 SPSSSSV 226

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RESULT 20
Q13239          PRELIMINARY;      PRT;      276 AA.
AC Q13239;

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DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Putative SRC-1-like adapter protein (SLAP) (SRC-like-adapter).
GN SLAP.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OK NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96423054; PubMed=8825655;
RA Angrist M., Wells D.E., Chakravarti A., Pandey A.;
RT "Chromosomal localization of the mouse Src-like adapter protein (Slap)
RT gene and its putative human homolog SLA";
RL Genomics 30:623-625(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RA Melferink P.H.S., Zorn G., Blikker H., Bolhuis P.A., Baas F.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Ohtsuka T., Hatake K., Ikeda M., Tomizuka H., Terui Y., Uwai M.,
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Blechschmidt K., Kalaydjieva L., Goodman R., Greenham D., Baas F.,
RA Junges R., Schilhabel M., Wen G., Menzel U., Detle M., Baumgart C.,
RA Rosenthal A.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=BONE MARROW;
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC - - SIMILARITY: CONTAINS 1 SH3 DOMAIN.
DR EMBL; U30473; AAC50357.1; -
DR EMBL; U44403; AAC27662.1; -
DR EMBL; D89077; BAA13758.1; -
DR EMBL; AF305872; AAC17933.1; -
DR EMBL; BC007042; AA07042.1; -
DR HSSP; P08631; 3HCK.
DR InterPro: IPR000980; SH2.
DR InterPro: IPR001452; SH3.
DR Pfam; PF00017; SH2_1.
DR Pfam; PF00018; SH3_1.
DR PRINTS; PR00401; SH2DOMAIN.
DR ProDom; PD000093; SH2_1.
DR SMART; SM00252; SH2; 1.
DR SMART; SM00326; SH3; 1.
DR PROSITE; PS50001; SH2; 1.
DR PROSITE; PS50002; SH3; 1.
KM SH3 domain. 276 AA; 31156 MW; B0FCC7D7B2ECA378 CRC64;
SQ SEQUENCE

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Query Match          3.1%; Score 8; DB 4; Length 276;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 159 YISPLTF 166
DB 143 YISPLTF 150

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RESULT 21
O8QZX8          PRELIMINARY;      PRT;      280 AA.
ID O8QZX8;
AC O8QZX8;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

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RESULT 24
063789 PRELIMINARY; PRT; 461 AA.
AC 063789;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Phosphatidylinositol 3-kinase regulatory gamma subunit (PI3-Kinase
DE p55-gamma subunit) (P55PIK) (p55-gamma).
GN PI3K3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxId=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WISTER; TISSUE=BRAIN;
RX MEDLINE=96214979; PubMed=8621382;
RA Inukai K., Anai M., VanBreda E., Hosaka T., Katagiri H., Funaki M.,
RA Fukuhara Y., Ogihara T., Yazaki Y., Kikuchi M., Oka Y., Asano T.;
RT "A novel 55-kDa regulatory subunit for phosphatidylinositol 3-kinase
RT structurally similar to p55PIK is generated by alternative splicing of
RT the p55alpha gene."
RL J. Biol. Chem. 271:5317-5320 (1996).
CC -1- FUNCTION: BINDS TO ACTIVATED (PHOSPHORYLATED) PROTEIN-TYROSINE
CC KINASES THROUGH ITS SH2 DOMAIN AND REGULATES THEIR KINASE
CC ACTIVITY. DURING INSULIN STIMULATION, IT ALSO BINDS TO IRS-1.
CC -1- SUBUNIT: HETERODIMER OF A P110 (CATALYTIC) AND A P55 (REGULATORY)
CC SUBUNITS.
CC -1- TISSUE SPECIFICITY: HIGHEST LEVELS IN BRAIN AND TESTIS. LOWER
CC LEVELS IN ADIPOSE TISSUE, KIDNEY, HEART, LUNG AND SKELETAL MUSCLE.
CC BARELY DETECTABLE IN LIVER AND SPLEEN.
CC -1- SIMILARITY: CONTAINS 2 SH2 DOMAINS.
CC -1- SIMILARITY: HIGH, WITH OTHER P55 SUBUNITS, AND WITH P85-ALPHA AND
CC P85-BETA SUBUNITS.
DR EMBL: D64047; BAA10927.1; -.
DR HSSP: P23727; 2PMB.
DR InterPro: IPR001720; PI3kinase_P85.
DR InterPro: IPR000980; SH2.
DR Pfam: PF00017; SH2; 2.
DR PRINTS: PR00678; PI3KINASEP85.
DR PRODOM: PD000093; SH2; 2.
DR SMART: SM00252; SH2; 2.
DR PROSITE: PS50001; SH2; 2.
DR SH2 domain; Phosphorylation.
FT DOMAIN 65 163 SH2.
FT MOD_RES 341 455 SH2.
FT MOD_RES 341 341 PHOSPHORYLATION (BY SIMILARITY).
SQ SEQUENCE 461 AA; 54254 MW; 6467DB8447CC562B CRC64;

Query Match 3.1%; Score 8; DB 11; Length 461;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 116 GAFLRES 123
DB 378 GAFLRES 385

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RP SEQUENCE FROM N.A.
RC STRAIN=UCI;
RX MEDLINE=20408254; PubMed=10951585;
RA Miller M.A., Malik I.A., Shenk M.A., Steele R.E.;
RT "The Src/Csk regulatory circuit arose early in metazoan evolution."
RT Oncogene 19:3925-3930 (2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=UCI;
RA Steele R.E.;
RX MEDLINE=9627775; AAC35011.1; -.
CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
DR EMBL: AF067775; AAC35011.1; -.
DR HSSP: P41240; 1CSK.
DR InterPro: IPR00719; Euk_pkinase.
DR InterPro: IPR000980; SH2.
DR InterPro: IPR001452; SH2.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00069; pkinase; 1.
DR Pfam: PF00017; SH2; 1.
DR Pfam: PF00018; SH3; 1.
DR PRINTS: PR00401; SH2DOMAIN.
DR PRODOM: PD000001; Euk_pkinase; 1.
DR PRODOM: PD000066; SH3; 1.
DR PRODOM: PD000093; SH2; 1.
DR SMART: SM00252; SH2; 1.
DR SMART: SM00326; SH3; 1.
DR SMART: SM00219; TYRK; 1.
DR PROSITE: PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE: PS50011; PROTEIN KINASE DOM; 1.
DR PROSITE: PS00109; PROTEIN KINASE_TYR; 1.
DR PROSITE: PS50001; SH2; 1.
DR PROSITE: PS50002; SH3; 1.
DR ATP-binding; Kinase; Receptor; SH3 domain; Transferase;
KW Tyrosine-protein kinase.
SQ SEQUENCE 467 AA; 53349 MW; 64A55016B855F2F CRC64;

Query Match 3.1%; Score 8; DB 5; Length 467;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 101 REKAEEL 108
DB 99 REKAEEL 106

RESULT 26
013064 PRELIMINARY; PRT; 488 AA.
AC 013064;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Lyn protein tyrosine kinase.
GN LYN.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxId=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Fukami Y., Funahiki K., Sato K.;
RT "Nucleotide sequence of Xenopus Lyn protein tyrosine kinase."
RT Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
DR EMBL: AB003358; BAA20078.1; -.
DR HSSP: P08631; 1AD5.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR000980; SH2.
DR InterPro: IPR001452; SH2.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00069; pkinase; 1.

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DR Pfam; PF00017; SH2; 1.
 DR Pfam; PF00018; SH3; 1.
 DR PRINTS; PR00401; SH2DOMAIN.
 DR PRINTS; PR00452; SH3DOMAIN.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Euk_kinase; 1.
 DR ProDom; PD000066; SH3; 1.
 DR ProDom; PD000093; SH2; 1.
 DR SMART; SM00252; SH2; 1.
 DR SMART; SM00326; SH3; 1.
 DR SMART; SM00219; TyKc; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS50002; SH3; 1.
 DR ATP-binding; Kinase; SH3 domain; Transferase; Tyrosine-protein kinase.
 SQ SEQUENCE 488 AA; 55794 MW; 87670688BEA9282 CRC64;

Query Match 3.1%; Score 8; DB 13; Length 488;
 Best Local Similarity 100.0%; Pred. No. 29;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 116 GAFLRES 123
 DB 127 GAFLRES 134

RESULT 27
 Q94AV6 PRELIMINARY; PRT; 499 AA.
 AC Q94AV6;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE ATG38500/F20M13_60.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC Eucosida II; Brassicales; Brassicaceae; Arabidopsis.
 NC NCB1_TaxId=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kim C.J., Chen H., Cheuk R., Koesema E., Meyers M.C., Banh J.,
 RA Bowser L., Carninci P., Dale J.M., Gibson H.A., Goldsmith A.D.,
 RA Hayashizaki Y., Iehida J., Jiang P.X., Jones T., Kamiya A.,
 RA Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X.,
 RA Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J.,
 RA Pham P.K., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,
 RA Tang C.C., Toriumi M., Yamada K., Yu G., Yu S., Shinzaki K.,
 RA Davis R.W., Theologis A., Ecker J.R.;
 RT "Arabidopsis cDNA clones";
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY045693; AAK74051.1;
 DR InterPro; IPR002198; ADH short.
 DR PROSITE; PS00061; ADH_SHORT; UNKNOWN 1.
 SQ SEQUENCE 499 AA; 57761 MW; 8766745023E1B3B CRC64;

Query Match 3.1%; Score 8; DB 10; Length 499;
 Best Local Similarity 100.0%; Pred. No. 30;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 131 SLVSLR 138
 DB 8 SLVSLR 15

RESULT 28
 Q9DDK6 PRELIMINARY; PRT; 502 AA.
 AC Q9DDK6;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)

DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Src-family tyrosine kinase SCK.
 OS Salmo salar (Atlantic salmon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Cyprinodontiformes; Salmoniformes; Salmonidae; Salmo.
 NC NCB1_TaxId=8030;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hardvick I., Male R.;
 RT "A leukocyte cDNA of Atlantic salmon encoding a Src-family tyrosine kinase."
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
 DR EMBL; AF221110; AAG38611.1; -.
 DR HSSP; P08631; IAD5.
 DR InterPro; IPR000719; Euk_kinase.
 DR InterPro; IPR002290; Ser_thr_kinase.
 DR InterPro; IPR000980; SH2.
 DR InterPro; IPR001452; SH3.
 DR InterPro; IPR001245; Tyr_kinase.
 DR Pfam; PF00069; kinase; 1.
 DR Pfam; PF00017; SH2; 1.
 DR Pfam; PF00018; SH3; 1.
 DR PRINTS; PR00401; SH2DOMAIN.
 DR PRINTS; PR00452; SH3DOMAIN.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Euk_kinase; 1.
 DR ProDom; PD000066; SH3; 1.
 DR ProDom; PD000093; SH2; 1.
 DR SMART; SM00252; SH2; 1.
 DR SMART; SM00326; SH3; 1.
 DR SMART; SM00220; S_TKc; 1.
 DR SMART; SM00219; TyKc; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS50002; SH3; 1.
 DR ATP-binding; Kinase; SH3 domain; Transferase.
 KW SEQUENCE 502 AA; 56600 MW; 82DF0677AA99980 CRC64;
 SQ SEQUENCE 502 AA; 56600 MW; 82DF0677AA99980 CRC64;

Query Match 3.1%; Score 8; DB 13; Length 502;
 Best Local Similarity 100.0%; Pred. No. 30;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 128 GSVSLR 135
 DB 153 GSVSLR 160

RESULT 29
 Q62662 PRELIMINARY; PRT; 506 AA.
 AC Q62662;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Src related tyrosine kinase.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NC NCB1_TaxId=10116;
 RN [1]
 RP SEQUENCE OF 356-416 FROM N.A.
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=SMALL INTESTINE;
 RA MEDLINE=94220493; PubMed=8167158;
 RA Smith I., Avigan M.I.;
 RT "A newly identified tyrosine kinase is preferentially expressed in the gastrointestinal tract."
 RL Biochim. Biophys. Acta, Gene Struct. Expr. 1221:348-352(1994).
 RN [2]
 RP SEQUENCE FROM N.A.

RC STRAIN=SPRAGUE-DAWLEY; TISSUE=SMALL INTESTINE;
 MEDLINE=9633034; Pubmed=8760296;
 RA Smitha I.; Avigan M.I.;
 RT "The apical membranes of maturing gut columnar epithelial cells
 RT contain the enzymatically active form of a newly identified fyn-
 RT related tyrosine kinase.";
 RU Oncogene 13:547-559(1996).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=SMALL INTESTINE;
 RA Avigan M.I.;
 RU Submitted (MAY-1994) to the EMBL/Genbank/DBJ databases.
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
 DR EMBL: U09583; AAC52725.1; -.
 DR HSSP: P00523; 2PTK.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR000980; SH2.
 DR InterPro: IPR001452; SH3.
 DR InterPro: IPR001245; Tyr_pkinase.
 DR Pfam: PF00069; Pkinase; 1.
 DR Pfam: PF00017; SH2; 1.
 DR Pfam: PF00019; SH3; 1.
 DR PRINTS: PR00401; SH2DOMAIN.
 DR PRINTS: PR00452; SH3DOMAIN.
 DR PRINTS: PR00109; TYRKINASE.
 DR ProDom: PD000001; Euk_pkinase; 1.
 DR ProDom: PD000066; SH3; 1.
 DR ProDom: PD000093; SH2; 1.
 DR SMART: SMO0252; SH2; 1.
 DR SMART: SMO0326; SH3; 1.
 DR SMART: SMO0219; TyKc; 1.
 DR PROSITE: PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE: PS0011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE: PS50001; SH2; 1.
 DR PROSITE: PS50002; SH3; 1.
 KW ATP-binding; Kinase; SH3 domain; Transferase; Tyrosine-protein kinase.
 SQ SEQUENCE 506 AA; 58166 MW; 69F471DE4F74D82 CRC64;

Query Match 3.1%; Score 8; DB 11; Length 506;
 Best Local Similarity 100.0%; Pred. No. 30;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 116 GAFLIRES 123
 Db 139 GAFLIRES 146

RESULT 30
 ID 061364 PRELIMINARY; PRT; 512 AA.
 AC 061364;
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
 DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
 DE Protein tyrosine kinase.
 GN FRK OR BSK.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=95137395; Pubmed=7835707;
 RA Oberg-Welsh C. Welsh M.; a murine FRK homologue with a specific pattern of
 RT tissue distribution.";
 RL Gene 152:239-242(1995).
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
 DR EMBL: L36132; AAA65197.1; -.
 DR HSSP: P00523; 2PTK.
 DR MGD: MGI:103265; Frk.
 DR InterPro: IPR000719; Euk_pkinase.

DR InterPro: IPR000980; SH2.
 DR InterPro: IPR001452; SH3.
 DR InterPro: IPR001245; Tyr_pkinase.
 DR Pfam: PF00069; Pkinase; 1.
 DR Pfam: PF00017; SH2; 1.
 DR Pfam: PF00019; SH3; 1.
 DR PRINTS: PR00401; SH2DOMAIN.
 DR PRINTS: PR00452; SH3DOMAIN.
 DR ProDom: PD000001; Euk_pkinase; 1.
 DR ProDom: PD000066; SH3; 1.
 DR ProDom: PD000093; SH2; 1.
 DR SMART: SMO0252; SH2; 1.
 DR SMART: SMO0326; SH3; 1.
 DR SMART: SMO0219; TyKc; 1.
 DR PROSITE: PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE: PS0011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE: PS50001; SH2; 1.
 DR PROSITE: PS50002; SH3; 1.
 KW ATP-binding; Kinase; SH3 domain; Transferase; Tyrosine-protein kinase.
 SQ SEQUENCE 512 AA; 58892 MW; 4D9DBDAD01997E95 CRC64;

Query Match 3.1%; Score 8; DB 11; Length 512;
 Best Local Similarity 100.0%; Pred. No. 31;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 116 GAFLIRES 123
 Db 145 GAFLIRES 152

RESULT 31
 ID 061745 PRELIMINARY; PRT; 512 AA.
 AC 061745;
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
 DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
 DE Intestinal tyrosine kinase.
 GN FRK OR IYK.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/C; TISSUE=MAMMARY GLAND;
 RX MEDLINE=95251566; Pubmed=7733928;
 RA Thiverson M., Albrecht D., Zuercher G., Andres A., Ziemiecki A.;
 RT "IYK, a novel intracellular protein tyrosine kinase differentially
 RT expressed in the mouse mammary gland and intestine.";
 RL Blochem. Biophys. Res. Commun. 209:582-589(1995).
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
 DR EMBL: Z48757; CA88658.1; -.
 DR HSSP: P00523; 2PTK.
 DR MGD: MGI:103265; Frk.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR000980; SH2.
 DR InterPro: IPR001452; SH3.
 DR InterPro: IPR001245; Tyr_pkinase.
 DR Pfam: PF00069; Pkinase; 1.
 DR Pfam: PF00017; SH2; 1.
 DR Pfam: PF00019; SH3; 1.
 DR PRINTS: PR00401; SH2DOMAIN.
 DR PRINTS: PR00452; SH3DOMAIN.
 DR ProDom: PD000001; Euk_pkinase; 1.
 DR ProDom: PD000066; SH3; 1.
 DR ProDom: PD000093; SH2; 1.
 DR SMART: SMO0252; SH2; 1.
 DR SMART: SMO0326; SH3; 1.
 DR SMART: SMO0219; TyKc; 1.

DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS50001; SH2; 1.
 DR PROSITE; PS50002; SH3; 1.
 KW ATP-binding; Kinase; SH3 domain; Transferase; Tyrosine-protein kinase.
 SQ SEQUENCE 512 AA; 58928 MW; 910D7F27C9BBB3FD CRC64;

Query Match
 Best Local Similarity 100.0%; Score 8; DB 11; Length 512;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 116 GAFLIRES 123
 |||||
 Db 145 GAFLIRES 152

RESULT 32
 0922K9
 ID 0922K9 PRELIMINARY; PRT; 512 AA.
 AC 0922K9
 DT 01-DEC-2001 (TEMBLrel. 19, Created)
 DT 01-DEC-2001 (TEMBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (TEMBLrel. 21, Last annotation update)
 DE B-cell src-homology tyrosine kinase.
 GN FRK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NC NCB1_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strauberg R.;
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC007137; AA07137.1; -.
 DR MGD; MGI:103265; Frk.
 DR InterPro; IPR000719; Euk_pkinase.
 DR InterPro; IPR000980; SH2.
 DR InterPro; IPR01452; SH3.
 DR InterPro; IPR01245; Tyr_pkinase.
 DR Pfam; PF00069; pkinase; 1.
 DR Pfam; PF00017; SH2; 1.
 DR Pfam; PF00018; SH3; 1.
 DR ProDom; PD000001; Euk_pkinase; 1.
 DR ProDom; PD000066; SH3; 1.
 DR ProDom; PD000093; SH2; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; UNKNOWN_1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; UNKNOWN_1.
 DR PROSITE; PS50001; SH2; 1.
 DR PROSITE; PS50002; SH3; 1.
 KW ATP-binding; Kinase; Transferase.
 SQ SEQUENCE 512 AA; 58843 MW; B79A0BC07B9EC5F8 CRC64;

Query Match
 Best Local Similarity 100.0%; Score 8; DB 11; Length 512;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 116 GAFLIRES 123
 |||||
 Db 145 GAFLIRES 152

RESULT 33
 063206
 ID 063206 PRELIMINARY; PRT; 517 AA.
 AC 063206;
 DT 01-NOV-1996 (TEMBLrel. 01, Created)
 DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
 DT 01-MAR-2002 (TEMBLrel. 20, Last annotation update)
 DE FRK protein.
 GN FRK.
 OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NC NCB1_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=F344; TISSUE=LEUKEMIA;
 RA Yue C.C., Labash J.D., Jaffe M.;
 RT "Nucleotide and deduced amino acid sequence of rat FRK";
 RL Nucleic Acids Res. 0:0-0(1990).
 CC -1 SIMILARITY: CONTAINS 1 SH3 DOMAIN.
 DR EMBL; X57018; CAA40337.1; -.
 DR HSSP; P00523; 2PTK.
 DR InterPro; IPR000719; Euk_pkinase.
 DR InterPro; IPR000980; SH2.
 DR InterPro; IPR01452; SH3.
 DR InterPro; IPR01245; Tyr_pkinase.
 DR Pfam; PF00069; pkinase; 1.
 DR Pfam; PF00017; SH2; 1.
 DR Pfam; PF00018; SH3; 1.
 DR PRINTS; PR00401; SH2DOMAIN.
 DR PRINTS; PR00452; SH3DOMAIN.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Euk_pkinase; 1.
 DR ProDom; PD000066; SH3; 1.
 DR ProDom; PD000093; SH2; 1.
 DR SMART; SM00252; SH2; 1.
 DR SMART; SM00326; SH3; 1.
 DR SMART; SM00219; TYRK; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS50001; SH2; 1.
 DR PROSITE; PS50002; SH3; 1.
 KW ATP-binding; SH3 domain; Transferase; Tyrosine-protein kinase.
 SQ SEQUENCE 517 AA; 58792 MW; 852F8F3778C403F CRC64;

Query Match
 Best Local Similarity 100.0%; Score 8; DB 11; Length 517;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 116 GAFLIRES 123
 |||||
 Db 154 GAFLIRES 161

RESULT 34
 08WZ33
 ID 08WZ33 PRELIMINARY; PRT; 697 AA.
 AC 08WZ33;
 DT 01-MAR-2002 (TEMBLrel. 20, Created)
 DT 01-MAR-2002 (TEMBLrel. 20, Last sequence update)
 DT 01-MAR-2002 (TEMBLrel. 20, Last annotation update)
 DE Hypothetical 75.6 kDa protein.
 GN B916.60.
 OS Neurospora crassa.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariales; Sordariaceae; Neurospora.
 NC NCB1_TaxID=5141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Schulte U., Aign V., Hohelsel J., Brandt P., Fartmann B., Holland R.,
 RA Nyakatura G., Mewes H.W., Mannhaupt G.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA German Neurospora genome project;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL670003; CAD21241.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 697 AA; 75599 MW; 5371CC36A9657FC9 CRC64;

Query Match
 Best Local Similarity 100.0%; Score 8; DB 3; Length 697;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 PPSPLSS 19
|||||
Db 558 PPSPLSS 565

RESULT 35

ID P87122 PRELIMINARY; PRT; 743 AA.

AC P87122; (TREMblrel. 06, Created)
DT 01-JUN-1998 (TREMblrel. 06, Last sequence update)
DT 01-JUN-1998 (TREMblrel. 20, Last annotation update)
DE Hypothetical 82.4 kDa protein C3A12.06C in chromosome I.
OS SPAC3A12.06C.
OC Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OC NCBI_TaxID=4896;
ON (1)
RN [1]
RP SEQUENCE FROM N.A.

RA Subcock K., Churcher C.M., Wood V., Barrell B.G., Rajandream M.A.;
Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC -1- SIMILARITY: SOME TO C.ELEGANS C07A9.11 AND YEAST YJR106W.

DR EMBL; Z55395; CAB08751.1; -.
DR InterPro; IPR004837; NaCa_Ex; 2.
DR Pfam; PF01699; Na_Ca_Ex; 2.
KW Hypothetical protein; Transmembrane.

FT TRANSMEM 133 POTENTIAL.
FT TRANSMEM 109 129 POTENTIAL.
FT TRANSMEM 138 158 POTENTIAL.
FT TRANSMEM 183 203 POTENTIAL.
FT TRANSMEM 217 237 POTENTIAL.
FT TRANSMEM 239 259 POTENTIAL.
FT TRANSMEM 480 500 POTENTIAL.
FT TRANSMEM 528 548 POTENTIAL.
FT TRANSMEM 551 571 POTENTIAL.
FT TRANSMEM 580 600 POTENTIAL.
FT TRANSMEM 609 629 POTENTIAL.
FT TRANSMEM 649 669 POTENTIAL.
FT TRANSMEM 690 710 POTENTIAL.
FT TRANSMEM 718 738 POTENTIAL.
SQ SEQUENCE 743 AA; 82396 MW; 1585FD26FACFB8B8 CRC64;

Query Match 3.1%; Score 8; DB 3; Length 743;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 LPPSPLSS 18
|||||
Db 455 LPPSPLSS 462

RESULT 36

ID 09FFK6 PRELIMINARY; PRT; 810 AA.

AC 09FFK6; (TREMblrel. 16, Created)
DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)
DE Genomic DNA, chromosome 5, pl clone: MJ3.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Rosidae;
OC Eucosids II; Brassicales; Brassicaceae; Arabidopsids.
ON NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;

RX MEDLINE=97471969; PubMed=9330910;
RA Sato S., Kotani H., Nakamura Y., Kaneko T., Asamizu E., Fukami M.,
RA Miyajima N., Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. I. Sequence
RT features of the 1.6 Mb regions covered by twenty physically assigned
RT pl clones".
RL DNA Res. 4:215-230(1997).
DR EMBL; AB005237; BAB09662.1; -.
SQ SEQUENCE 810 AA; 89730 MW; 79E20A5E48BDF069 CRC64;

Query Match 3.1%; Score 8; DB 10; Length 810;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 LSLRLGP 58
|||||
Db 77 LSLRLGP 84

RESULT 37

ID 09BL20 PRELIMINARY; PRT; 827 AA.

AC 09BL20; (TREMblrel. 17, Created)
DT 01-JUN-2001 (TREMblrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Hypothetical 96.6 kDa protein.
GN Y4868A.10.
OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
ON NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN=BRISTOL N2;
RX MEDLINE=99069613; PubMed=9851916;
RA Waterston R.;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.

RC STRAIN=BRISTOL N2;
RA Murray J., Du H.;
RT "The sequence of C. elegans cosmid Y4868A.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.

RC STRAIN=BRISTOL N2;
RA Waterston R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC025721; AAK29901.2; -.
KW Hypothetical protein.
SQ SEQUENCE 827 AA; 96579 MW; 69D297E3446FC27 CRC64;

Query Match 3.1%; Score 8; DB 5; Length 827;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 140 ASMDRIRH 147
|||||
Db 14 ASMDRIRH 21

RESULT 38

ID 09GZT7 PRELIMINARY; PRT; 17 AA.

AC 09GZT7; (TREMblrel. 16, Created)
DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)
DE OGG1 type 1h (OGG1 type 1d) (Fragment).
ON OGG1 TYPE 1h OR OGG1 TYPE 1d.
GN

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OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCB1_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20184065; PubMed=10717238;
RA Shimura K., Kohno T., Takeuchi-Sasaki M., Maeda M., Segawa T.,
RA Kamo T., Sugimura H., Yokota J.;
RT "Expression of the OGG1-type 1a (nuclear form) protein in cancerous
RT and non-cancerous human cells.";
RL Int. J. Oncol. 16:701-707(2000).
DR EMBL; AB037882; BAB13297.1; -.
FT NON TER 1
SQ SEQUENCE 17 AA; 1748 MW; 824F34170BF91EF CRC64;

Query Match 2.7%; Score 7; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 166 FPSLOAL 172
Db 8 FPSLOAL 14

RESULT 39
O9HCR6 PRELIMINARY; PRT; 40 AA.
AC O9HCR6;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DE OGG1 type 1g (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCB1_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20184065; PubMed=10717238;
RA Shimura K., Kohno T., Takeuchi-Sasaki M., Maeda M., Segawa T.,
RA Kamo T., Sugimura H., Yokota J.;
RT "Expression of the OGG1-type 1a (nuclear form) protein in cancerous
RT and non-cancerous human cells.";
RL Int. J. Oncol. 16:701-707(2000).
DR EMBL; AB037881; BAB13296.1; -.
FT NON TER 1
SQ SEQUENCE 40 AA; 4380 MW; 4BDB53CAF26C64B3 CRC64;

Query Match 2.7%; Score 7; DB 4; Length 40;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 166 FPSLOAL 172
Db 8 FPSLOAL 14

RESULT 40
O9HCR7 PRELIMINARY; PRT; 61 AA.
AC O9HCR7;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DE OGG1 type 1f (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCB1_TaxID=9606;

OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCB1_TaxID=9606;

RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20184065; PubMed=10717238;
RA Shimura K., Kohno T., Takeuchi-Sasaki M., Maeda M., Segawa T.,
RA Kamo T., Sugimura H., Yokota J.;
RT "Expression of the OGG1-type 1a (nuclear form) protein in cancerous
RT and non-cancerous human cells.";
RL Int. J. Oncol. 16:701-707(2000).
DR EMBL; AB037880; BAB13295.1; -.
FT NON TER 1
SQ SEQUENCE 61 AA; 6729 MW; 11CBF7290828F6F3 CRC64;

Query Match 2.7%; Score 7; DB 4; Length 61;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 166 FPSLOAL 172
Db 8 FPSLOAL 14

RESULT 41
O9LWU9 PRELIMINARY; PRT; 70 AA.
AC O9LWU9;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DE Asparagine synthetase (Fragment).
OS Pyrus pyrifolia (Japanese pear) (Pyrus serotina).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC Eustoids I; Rosales; Rosaceae; Maloideae; Pyrus.
OX NCB1_TaxID=3767;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=CV. KIKUSUI; TISSUE=FRUIT;
RA Itai A., Tanaka K., Tanura F.;
RT "Pyrus pyrifolia ripening associated mRNA, clone pPFRU32.";
RL Submitted (DEC-1998) to the EMBL/Genbank/DBJ databases.
DR EMBL; AB021793; BAA96452.1; -.
FT NON TER 1
SQ SEQUENCE 70 AA; 7156 MW; 520F705CA1AE729 CRC64;

Query Match 2.7%; Score 7; DB 10; Length 70;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 35 ATVALG 41
Db 10 ATVALG 16

RESULT 42
O9PSJ0 PRELIMINARY; PRT; 93 AA.
AC O9PSJ0;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DE ZN-MYC oncoprotein (Fragment).
OS Brachydanio rerio (zebrafish) (zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCB1_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9323639; PubMed=8474440;
RA Schreiber-Agus N., Horner J., Torres R., Chiu F.C., Depinho R.A.;
RT "Zebra fish myc family and max genes: differential expression and
oncogenic activity throughout vertebrate evolution.";

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RL Mol. Cell. Biol. 13:2765-2775(1993).
 DR InterPro: IPR002418; Trp_Myc.
 DR Pfam: PF01056; Myc_N term.1.
 SO SEQUENCE 93 AA; 9811 MW; 84409B81CB5BE086 CRC64;

Query Match 2.7%; Score 7; DB 13; Length 93;
 Best Local Similarity 100.0%; Pred. No. 65;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 106 ELLPLPG 112
 |||||
 Db 52 ELLPLPG 58

RESULT 43
 O9C7L8 PRELIMINARY; PRT; 96 AA.

AC O9C7L8; 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE Hypothetical 10.5 KDa protein.
 GN F14C21.32.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC euroside II; Brassicales; Brassicaceae; Arabidopsids.
 CX NCBI_Taxid=3702;

RA [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RX MEDLINE=21016719; PubMed=1130712;
 RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
 White O., Alonso J., Altati H., Araujo R., Bowman C.L., Brookes S.Y.,
 Buehler E., Chan A., Chao Q., Chen H., Chuk R.F., Chin C.W.,
 Chung M.K., Conn L., Conway A.B., Conway A.R., Cressy T.H., Dewar K.,
 Dunn P., Egu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
 Gail J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizier L.,
 Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
 Kim C.J., Koo H.L., Kremetskaia I., Kurtz D.B., Kwan A., Lam B.,
 Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
 Lin X., Liu S.X., Liu Z.A., Luros J.S., Malt R., Marzilli A.,
 Maltischer J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
 Paig G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
 Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
 Sun H., Tallon L.J., Tamunga G., Toriumi W.J., Town C.D., Walker M.,
 Uterback T., Van Aken S., Vayberg M., Vysotskaia V.S., Walker M.,
 Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
 RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
 thaliana."
 RL Nature 408:816-820(2000).
 DR EMBL: AC069144; AAC5113.1; -.
 KW Hypothetical protein.
 SO SEQUENCE 96 AA; 10525 MW; 75B6C51B29468A39 CRC64;

Query Match 2.7%; Score 7; DB 10; Length 96;
 Best Local Similarity 100.0%; Pred. No. 67;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 168 SLOALVD 174
 |||||
 Db 62 SLOALVD 68

RESULT 44
 O8WUD9 PRELIMINARY; PRT; 102 AA.

AC O8WUD9; 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE Similar to RIKEN cDNA 1200014N16 gene.
 OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 CX NCBI_Taxid=9606;

RA [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=TESTIS;
 RA Strausberg R.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC020784; AAH20784.1; -.
 SO SEQUENCE 102 AA; 10778 MW; 18C9E173F4FB939D CRC64;

Query Match 2.7%; Score 7; DB 4; Length 102;
 Best Local Similarity 100.0%; Pred. No. 71;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 192 VLQRAP 198
 |||||
 Db 40 VLQRAP 46

RESULT 45
 Q55970 PRELIMINARY; PRT; 106 AA.

AC Q55970; 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE Hypothetical protein s110669.
 GN S110669.
 OS Synechocystis sp. (strain PCC 6803).
 OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
 CX NCBI_Taxid=1148;
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=96127529; PubMed=8590279;
 RA Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N.,
 Sugita M., Tabata S.;
 RT "Sequence analysis of the genome of the unicellular cyanobacterium
 Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb
 region from map positions 64k to 92k of the genome."
 RL DNA Res. 2:153-166(1995).
 RN [2]

RP SEQUENCE FROM N.A.
 RX MEDLINE=97061201; PubMed=8905231;
 RA Kaneko T., Sato S., Kotani H., Tanaka A., Asanizu E., Nakamura Y.,
 Miyajima N., Hirosewa M., Sugita M., Sasamoto S., Kimura T.,
 Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naito K., Okumura S.,
 Shimo S., Takeuchi C., Wada T., Watanabe A., Yamada M.,
 Tabata S.;
 RT "Sequence analysis of the genome of the unicellular cyanobacterium
 Synechocystis sp. strain PCC6803. II. Sequence determination of the
 RT entire genome and assignment of potential protein-coding regions."
 RL DNA Res. 3:109-136(1996).
 DR EMBL: D64005; BBA10747.1; -.
 KW Hypothetical protein; Complete proteome.
 SO SEQUENCE 106 AA; 12351 MW; 7FB81C429CE2493 CRC64;

Query Match 2.7%; Score 7; DB 16; Length 106;
 Best Local Similarity 100.0%; Pred. No. 74;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 13 SPSLSS 19
 |||||
 Db 85 SPSLSS 91

RESULT 46
 O9D4J0 PRELIMINARY; PRT; 109 AA.

AC O9D4J0; 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)

DE 4931430N09Rik protein.
 GN 4931430N09Rik.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=TESTIS;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamada I.,
 RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiya H.,
 RA Kuehl P., Lewis S., Mateno Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schiml L.W., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustinich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Momcharev P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Saeki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wyshew-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohlsuki S.,
 RA Hayashizaki Y.,
 RT "Functional annotation of a full-length mouse cDNA collection."
 RL Nature 409:685-690(2001).
 DR EMBL; AK016492; BAB30269.1; -
 DR MGD; MGI:1921613; 4931430N09Rik.
 SO SEQUENCE 109 AA; 13056 MW; A155B018F113E92 CRC64;
 QY 95 LYEGLSR 101
 DB 74 LYEGLSR 80
 RESULT 47
 ID Q95572 PRELIMINARY; PRT; 114 AA.
 AC Q95572;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Hypothetical protein PA0624.
 GN PA0624.
 OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 OC Pseudomonas.
 OX NCBI_TaxID=287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 15692 / PAOI;
 RX MEDLINE=20437337; PubMed=10984043;
 RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
 RA Hickey M.J., Brinkman F.S.L., Huftagle W.O., Kowalik D.J., Lagrou M.,
 RA Garber R.L., Goltry L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
 RA Brody L.A., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
 RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
 RA Reiter J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.,

RT "Complete genome sequence of Pseudomonas aeruginosa PAOI, an
 RT opportunistic pathogen."
 RL Nature 406:959-964(2000).
 DR EMBL; AB030825; BAA83162.1; -
 DR EMBL; AE004498; AAG04013.1; -
 KW Hypothetical protein; Complete proteome.
 SO SEQUENCE 114 AA; 12523 MW; 3C22EF61270DF50D CRC64;

Query Match 2.7%; Score 7; DB 16; Length 114;
 Best Local Similarity 100.0%; Pred. No. 79;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 134 VRLSRPA 140
 DB 20 VRLSRPA 26

RESULT 48
 ID Q8Y8M4 PRELIMINARY; PRT; 115 AA.
 AC Q8Y8M4;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DE Hypothetical protein lmo0778.
 GN LMO0778.
 OS Listeria monocytogenes.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
 OC Listeriaceae; Listeria.
 OX NCBI_TaxID=1639;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BGD-5 / SEROVAR 1/2A;
 RX MEDLINE=21537279; PubMed=11679669;
 RA Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
 RA Baquero F., Berche P., Bloecher H., Brandt P., Chakraborty T.,
 RA Charbit A., Cheouani F., Couve E., de Darvar A., Denoux P.,
 RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurge O.,
 RA Ertian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
 RA Gautier L., Goebel W., Gomez-Lopez N., Hahn T., Hauf J., Jackson D.,
 RA Jones L.-W., Kaerst U., Kreft J., Kunz M., Kunst F., Kurapkaj G.,
 RA Madueno E., Maitournam A., Mata Vicente J., Ng B., Nedjari H.,
 RA Nordstedt G., Novella S., de Pablo B., Perez-Diaz J.-C., Purcell R.,
 RA Remmel B., Rose M., Schluter T., Simoes N., Tierrez A.,
 RA Vazquez-Boland J.-A., Voss H., Wehland J., Cosset P.,
 RT "Comparative genomics of Listeria species."
 RL Science 294:849-852(2001).
 DR EMBL; AL591976; CAC98856.1; -
 DR Listeriac; LMO00778; -
 KW Hypothetical protein; Complete proteome.
 SO SEQUENCE 115 AA; 13596 MW; 5414CD46FD07531 CRC64;

Query Match 2.7%; Score 7; DB 16; Length 115;
 Best Local Similarity 100.0%; Pred. No. 79;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 144 RIRHYRI 150
 DB 64 RIRHYRI 70

RESULT 49
 ID Q9UFL7 PRELIMINARY; PRT; 117 AA.
 AC Q9UFL7;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DE Hypothetical protein 12.7 kDa protein.
 GN DKFZP34K058.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=TESTIS;
 RA O'Brienweilder B., Obermaier B., Mewes H.W., Gassenhuber J., Wiemann S.;
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL117583; CAB56005.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 117 AA; 12742 MW; 582E52156AE7BD29 CRC64;

Query Match 2.7%; Score 7; DB 4; Length 117;
 Best Local Similarity 100.0%; Pred. No. 81;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 164 LTRPSLQ 170
 |||||
 Db 34 LTRPSLQ 40

RESULT 50

092FH6 PRELIMINARY; PRT; 118 AA.
 ID 092FH6
 AC 092FH6;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Hypothetical protein lin0130.
 GN LIN0130.
 OS Listeria innocua.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
 OC Listeriaceae; Listeria.
 OX NCBI_TaxID=1642;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CLIP 11262 / SEROVAR 6A;
 RX PubMed=11679669;
 RA Glaeser P., Frangoul L., Buchrieser C., Rusniok C., Amend A.,
 Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,
 Charbit A., Cheouni F., Couve E., de Daruvar A., Dehoux P.,
 Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
 Ertan K.-D., Fshil H., Garcia-del Portillo F., Garrido P., Jackson D.,
 Jones L.-M., Kaerst U., Krell J., Kuhn M., Kunst F., Kurapkut G.,
 Madueno E., Maitounam A., Mata Vicente J., Ng E., Nedjari H.,
 Nordstiek G., Novella S., de Pablo B., Perez-Diaz J.-C., Purcell R.,
 Rammel B., Rose M., Schluter T., Simoes N., Tierrez A.,
 Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
 RT "Comparative genomics of Listeria species.";
 RL Science 294:849-852(2001).
 DR EMBL; AU596163; CAC93363.1; -.
 DR Listeriet; LIN00130; -.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 118 AA; 13930 MW; 9118528B7C1FAE5 CRC64;

Query Match 2.7%; Score 7; DB 16; Length 118;
 Best Local Similarity 100.0%; Pred. No. 81;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 144 RIRHYRI 150
 |||||
 Db 65 RIRHYRI 71

Search completed: March 24, 2003, 16:08:06
 Job time : 44 secs